



#7

Carp0089.ST25.txt

SEQUENCE LISTING

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<120> Biological Products

<130> Carp-0089

<140> 09/875,221

<141> 2001-06-06

<150> GB0013810.7

<151> 2000-06-06

<160> 130

<170> PatentIn version 3.1

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 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 gac cgg gtc acc atc act tgt aaa gcc agt cag aac gta ggt act aac 96
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
 20 25 30
 gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa gcc ctc atc 144
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
 35 40 45
 tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga 192
 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
 50 55 60
 tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca 240
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc 288
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
 85 90 95
 aca ttc ggt cag ggt act aaa gta gaa atc aaa 321
 Thr Phe Gly Gln Gly Thr Lys Val Ile Lys
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 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
 20 25 30
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
 35 40 45

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Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
 85 90 95

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1 5 10 15

gac cgg gtc acc atc act tgt aaa gcc agt cag aac gta ggt act aac 96
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
 20 25 30

gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa ctc ctc atc 144
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga 192
 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
 50 55 60

tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca 240
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc 288
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
 85 90 95

aca ttc ggt cag ggt act aaa gta gaa atc aaa 321
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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tcc gtc aaa gtt tcg tgt aag gcc tca ggc tac gtg ttc aca gac tat 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr
20 25 30

ggt atg aat tgg gtc aga cag gcc ccg gga caa ggc ctg gaa tgg atg 144
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

ggt tgg att aat act tac att gga gag cct att tat gct caa aag ttc 192
Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Gln Lys Phe
50 55 60

cag ggc aga gtc acg ttc act cta gac acc tcc aca agc act gca tac 240

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Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

atg gag ctg tca tct ctg aga tcc gag gac acc gca gtg tac tat tgt 288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gct aga gga tac aga tct tat gcc atg gac tac tgg ggc cag ggt acc 336
Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

cta gtc aca gtc tcc tca 354
Leu Val Thr Val Ser Ser
115

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
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Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
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 tca ctg aga ttg tcc tgt gct gca tct ggt tac gtc ttc aca gac tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr
 20 25 30
 gga atg aat tgg gtt aga cag gcc ccg gga aag ggc ctg gaa tgg atg 144
 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 ggt tgg att aat act tac att gga gag cct att tat gct gac agc gtc 192
 Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val
 50 55 60
 aag ggc aga ttc acg ttc tct cta gac aca tcc aag tca aca gca tac 240
 Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
 65 70 75 80
 ctc caa atg aat agc ctg aga gca gag gac acc gca gtg tac tat tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gct aga gga tac aga tct tat gcc atg gac tac tgg ggc cag ggt acc 336
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 20 25 30
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 35 40 45
 Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
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23

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<400> 21
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<210> 32
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<400> 33
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<400> 36
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<210> 44
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<210> 45
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gcagatgggc ccttcgttga ggctgmrgag acdgtga 37

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<400> 54
gctgacagac taacagactg ttcc 24

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<400> 55
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gaattcaggg tcaccatcac ttgtaaagcc agtcagaacg taggtactaa cgtagcctgg 60
tatcagcaaa 70

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<400> 57
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ccaggctacg t 71

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actgatttca c 71

<210> 59
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<212> DNA
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taccactacc g 71

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ttcaactgct catcagat 18

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at 62

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gtacactgcg gtgtcctc 78

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<223> Primer P7997

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 ggaggtatgc tgttgacttg gatgtgtcta gagagaacgt gaatctgccc ttgaa 55

<210> 80

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer P7998

<400> 80
 ccaagtcaac agcatacctc caaatgaata gcctgagagc agaggacacc gcagtgtact 60
 at 62

<210> 81

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer P7993

<400> 81
 gaattcggta ccctggcccc agtagtccat ggcataagat ctgtatcctc tagcacaata 60
 gtacactgcg gtgtcctc 78

<210> 82

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer P7996

<400> 82

gaattcgtgc actctgaggt tcagctgggc

30

<210> 83

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' Primer

<400> 83

cgcgcgcaa ttgcagtggc cttggctggt ttcgctaccg tagcgcaagc tgacattcaa

60

atgacccaga gccc

74

<210> 84

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' Primer

<400> 84

ttcaactgct catcagatgg

20

<210> 85

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' Primer

<400> 85

gctatcgcaa ttgcagtggc gctagctggt ttcgccaccg tggcgcaagc tgaggttcag

60

ctggtcgagt caggaggc

78

<210> 86

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' Primer

<400> 86

gcctgagttc cacgacac

18

<210> 87

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Group 1 consensus framework L1

<400> 87

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 88

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 framework L1

<400> 88

Ala Ser Pro Ile Leu Glu Val Ala Leu Met Glu Thr Thr His Arg Gly
1 5 10 15

Leu Asn Ser Glu Arg Gly Leu Asn Leu Tyr Ser Pro His Glu Met Glu
20 25 30

Thr Ser Glu Arg Thr His Arg Ser Glu Arg Val Ala Leu Gly Leu Tyr
35 40 45

Ala Ser Pro Ala Arg Gly Val Ala Leu Ser Glu Arg Val Ala Leu Thr
50 55 60

His Arg Cys Tyr Ser
65

<210> 89

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Human group 1 consensus framework L2

<400> 89

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 90

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 framework L2

<400> 90

Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Ala	Leu	Ile	Tyr
1				5					10					15

<210> 91

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Human group 1 consensus framework L3

<400> 91

Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys
			20					25					30		

<210> 92

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 framework L3

<400> 92

Gly	Val	Pro	Tyr	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Thr	Val	Gln	Ser	Glu	Asp	Leu	Ala	Glu	Tyr	Phe	Cys
			20					25					30		

<210> 93

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Human group 1 consensus framework L4

<400> 93

Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
1				5					10	

<210> 94

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 framework L4

<400> 94

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
1 5 10

<210> 95

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Human group 1 consensus framework H1

<400> 95

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

<210> 96

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 framework H1

<400> 96

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr
20 25 30

<210> 97

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Human group 1 consensus framework H2

<400> 97

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 98

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 framework H2

<400> 98

Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met Gly
1 5 10

<210> 99
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 1 consensus framework H3

<400> 99

Arg Val Thr Ile Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 100
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 framework H3

<400> 100

Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe Leu Gln
1 5 10 15

Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg
20 25 30

<210> 101
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 1 consensus framework H4

<400> 101

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 102
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 framework H4

<400> 102

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1 5 10

<210> 103
<211> 324
<212> DNA
<213> Murine

<220>
<221> CDS
<222> (1)..(324)
<223>

<400> 103
gac att gtg atg acc cag tct caa aaa ttc atg tcc aca tca gta gga 48
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15
gac agg gtc agc gtc acc tgc aag gcc agt cag aat gtg ggt act aat 96
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30
gta gcc tgg tat caa cag aaa cca gga caa tct cct aaa gca ctg att 144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
35 40 45
tac tcg gca tcc ttc cta tat agt gga gtc cct tat cgc ttc aca ggc 192
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Thr Gly
50 55 60
agt gga tct ggg aca gat ttc act ctc acc atc agc act gtg cag tct 240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Val Gln Ser
65 70 75 80
gaa gac ttg gca gag tat ttc tgt cag caa tat aac atc tat cct ctc 288
Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
85 90 95
acg ttc ggt gct ggg acc aag ctg gag ctg aaa cgt 324
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
100 105

<210> 104
<211> 108
<212> PRT
<213> Murine

<400> 104

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
35 40 45
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Thr Gly

50

55

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
100 105

<210> 105
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> hTNF40 heavy chain variable domain

<220>
<221> CDS
<222> (1)..(354)
<223>

<400> 105
cag atc cag ttg gtg cag tct gga cct gag ctg aag aag cct gga gag 48
Gln-Ile Gln Leu-Val Gln-Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15
aca gtc aag atc tcc tgc aag gct tct gga tat gtt ttc aca gac tat 96
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr
20 25 30
gga atg aat tgg gtg aag cag gct cca gga aag gct ttc aag tgg atg 144
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met
35 40 45
ggc tgg ata aac acc tac att gga gag cca ata tat gtt gat gac ttc 192
Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Val Asp Asp Phe
50 55 60
aag gga cga ttt gcc ttc tct ttg gaa acc tct gcc agc act gcc ttt 240
Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe
65 70 75 80
ttg cag atc aac aac ctc aaa aat gag gac acg gct aca tat ttc tgt 288
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95
gca aga ggt tac cgg tcc tat gct atg gac tac tgg ggt caa gga acc 336
Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110
tca gtc acc gtc tct tca 354
Ser Val Thr Val Ser Ser
115

<210> 106
<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 heavy chain variable domain

<400> 106

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr
 20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met
 35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Val Asp Asp Phe
 50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe
 65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
 85 90 95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Ser Val Thr Val Ser Ser
 115

<210> 107

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> OmpA oligonucleotide adaptor

<220>

<221> CDS

<222> (29)..(67)

<223>

<400> 107

tcgagttcta gataacgagg cgtaaaaa atg aaa aag aca gct atc gca att 52
 Met Lys Lys Thr Ala Ile Ala Ile
 1 5

gca gtg gcc ttg gct ctgacgtacg agtcagg 84
 Ala Val Ala Leu Ala
 10

<210> 108

<211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OmpA oligonucleotide adaptor

<400> 108

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala
 1 5 10

<210> 109
 <211> 67
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IGS cassette-1

<220>
 <221> CDS
 <222> (2)..(40)
 <223>

<220>
 <221> CDS
 <222> (43)..(66)
 <223>

<400> 109
 g agc tca cca gta aca aaa agt ttt aat aga gga gag tgt ta atg aag 48
 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Met Lys
 1 5 10 15

aag act gct ata gca att g 67
 Lys Thr Ala Ile Ala Ile
 20

<210> 110
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IGS cassette-1

<400> 110

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 1 5 10

<210> 111
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IGS cassette-1

<400> 111

Met Lys Lys Thr Ala Ile Ala Ile
 1 5

<210> 112

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> IGS cassette-2

<220>

<221> CDS

<222> (2)..(43)

<223>

<220>

<221> CDS

<222> (45)..(68)

<223>

<400> 112

g agc tca cca gta aca aaa agt ttt aat aga ggg gag tgt taa a atg 47
 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Met
 1 5 10

aag aag act gct ata gca att g 69
 Lys Lys Thr Ala Ile Ala Ile
 15 20

<210> 113

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> IGS cassette-2

<400> 113

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 1 5 10

<210> 114

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> IGS cassette-2

<400> 114

Met Lys Lys Thr Ala Ile Ala Ile
 1 5

<210> 115

<211> 81
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IGS cassette-3

<220>
 <221> CDS
 <222> (2)..(43)
 <223>

<220>
 <221> CDS
 <222> (57)..(80)
 <223>

<400> 115
 g agc tca cca gta aca aaa agc ttt aat aga gga gag tgt tga 43
 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 1 5 10

ggaggaaaaa aaa atg aag aaa act ggt ata gca att g 81
 Met Lys Lys Thr Ala Ile Ala Ile
 15 20

<210> 116
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IGS cassette-3

<400> 116
 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 1 5 10

<210> 117
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IGS cassette-3

<400> 117
 Met Lys Lys Thr Ala Ile Ala Ile
 1 5

<210> 118
 <211> 81
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IGS cassette-4

<220>
 <221> CDS
 <222> (2)..(43)
 <223>

<220>
 <221> CDS
 <222> (57)..(80)
 <223>

<400> 118
 g agc tca cca gta aca aaa agt ttt aat aga gga gag tgt tga 43
 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 1 5 10

cgaggattat ata atg aag aaa act gct ata gca att g 81
 Met Lys Lys Thr Ala Ile Ala Ile
 15 20

<210> 119
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IGS cassette-4

<400> 119
 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 1 5 10

<210> 120
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IGS cassette-4

<400> 120
 Met Lys Lys Thr Ala Ile Ala Ile
 1 5

<210> 121
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human group 3 consensus framework H1

<400> 121
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser

20

25

30

<210> 122

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Human group 3 consensus framework H2

<400> 122

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
 1 5 10

<210> 123

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Human group 3 consensus framework H3

<400> 123

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 20 25 30

<210> 124

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Human group 3 consensus framework H4

<400> 124

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 1 5 10

<210> 125

<211> 648

<212> DNA

<213> Artificial Sequence

<220>

<223> Grafted heavy chain for fab

<400> 125

gaggttcagc tggctcagtc aggaggcggc ctcgtgcagc ctggcggatc actgagattg 60

tcctgtgctg catctgggta cgtcttcaca gactatggaa tgaattgggt tagacaggcc 120

ccgggaaagg gcctggaatg gatggggttgg attaatactt acattggaga gcctatttat 180

gctgacagcg tcaagggcag attcacgttc tctctagaca catccaagtc aacagcatac 240

Carp0089.ST25.txt

ctccaatga atagcctgag agcagaggac accgcagtgt actattgtgc tagaggatac 300
 agatcttatg ccatggacta ctggggccag ggtaccctag tcacagtctc ctcagcttcc 360
 accaagggcc catcggtctt cccctggca ccctcctcca agagcacctc tgggggcaca 420
 gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tctacagtc ctcaggactc 540
 tactccctca gcagctggt gaccgtgcc tccagcagct tgggcaccca gacctacatc 600
 tgcaacgtga atcacaagcc cagcaacacc aaggtcgaca agaaagtt 648

<210> 126

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Grafted heavy chain for fab

<400> 126

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr
 - 20 - 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

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Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val
210 215

<210> 127

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Grafted light chain for fab and modified fab

<400> 127

gacattcaaa tgacccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc 60

atcacttgta aagccagtca gaacgtaggt actaacgtag cctggtatca gcaaaaacca 120

ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac 180

aggttcagcg gatccggtag tgggtactgat ttcaccctca cgatcagtag cctccagcca 240

gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag 300

ggtactaaag tagaaatcaa acgtacggtg gcggcccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaagggt gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcac cagtaacaaa aagctttaat agaggagagt gt 642

<210> 128

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Grafted light chain for fab and modified fab

<400> 128

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

Carp0089.ST25.txt

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 129

<211> 687

<212> DNA

<213> Artificial Sequence

<220>

<223> Grafted heavy chain for modified fab

<400> 129

gaggttcagc tggtcgagtc aggaggcgggt ctgctgcagc ctggcggatc actgagattg 60

tcctgtgctg catctgggta cgtcttcaca gactatggaa tgaattgggt tagacaggcc 120

ccgggaaagg gcctggaatg gatggggttg attaatactt acattggaga gcctatttat 180

gctgacagcg tcaagggcag attcacgttc tctctagaca catccaagtc aacagcatac 240
 ctccaaatga atagcctgag agcagaggac accgcagtgt actattgtgc tagaggatac 300
 agatcttatg ccatggacta ctggggccag ggtaccctag tcacagtctc ctcagcttcc 360
 accaagggcc catcggcttt ccccttgcca cctcctcca agagcacctc tgggggcaca 420
 ggggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccgctg tcctacagtc ctcaggactc 540
 tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacac 600
 tgcaacgtga atcacaagcc cagcaacacc aaggtcgaca agaaagtga gcccaaactc 660
 tgtgacaaaa ctcacacatg cgccgcg 687

<210> 130
 <211> 229
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Grafted heavy chain for modified fab

<400> 130

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

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Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Ala Ala
225